

10/528344

<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

<120> EXPRESSION SYSTEMS OF TOXIC PROTEINS, VECTORS
AND PROCESS FOR MANUFACTURING TOXIC PROTEINS

<130> B14143 EE

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<150> FR N°02 11676

<151> 2002-09-20

<160> 53

<170> PatentIn Ver. 2.1

<210> 1

<211> 37

<212> PRT

<213> Hepatitis C virus

<400> 1

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1 5 10 15

Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu Leu Phe
20 25 30

Ala Gly Val Asp Ala
35

<210> 2

<211> 31

<212> PRT

<213> Hepatitis C virus

<400> 2

Met Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val
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Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala
20 25 30

<210> 3

<211> 111

<212> DNA

<213> Hepatitis C virus

<400> 3

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aactggctca aagttcttgt tttctgctg ctgttcgctg gtgttgacgc t 111

<210> 4

<211> 93

<212> DNA

<213> Hepatitis C virus

<400> 4

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tggatgatgc tgctgatctc tcaggctgaa gct 93

B141431-PCT.txt

<210> 5
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pT7-7

<400> 5
gggaatgcca tatgatcgct ggtg

24

<210> 6
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (-) of insertion into pT7-7

<400> 6
gcatatcgat ctaagcgtca aca

23

<210> 7
<211> 131
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: TME1 coding sens DNA
+ 3' cla I site

<400> 7
atgccccatatg atcgctggtg ctcactgggg tggctggct ggtatcgctt acttctctat 60
ggttggtaac tgggctaaag ttctggttgt tctgctgctg ttcgctggtg ttgacgctta 120
gatcgatatg c 131

<210> 8
<211> 131
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: anticodant sens DNA
+ 5' cla I site

<400> 8
gcatatcgat ctaagcgtca acaccagcga acagcagcag aacaaccaga acttttagccc 60
agttaccaac catagagaag taagcgatac cagccagaac accccagtga gcaccagcga 120
tcatatggca t 131

<210> 9
<211> 74
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
coding sens oligonucleotide for the synthesis of
TME1

<400> 9
atgccccatatg atcgctggtg ctcactgggg tggctggct ggtatcgctt acttctctat 60

<210> 10
 <211> 79
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 anticoding sens oligonucleotide for the synthesis of
 TME1

<400> 10
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 agttaccaac catagagaa 79

<210> 11
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide (+) of insertion into pGEXKT without
 the dp site

<400> 11
 ggatccatgg aatacgttgt tc 22

<210> 12
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide (+) of insertion into pGEXKT with
 the dp site

<400> 12
 ggatccgacc cgatggaata cgttgttc 28

<210> 13
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide (-) of insertion into pGEXKT

<400> 13
 gaattcctaa gtttcagcct gag 23

<210> 14
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide (+) of transfert onto pET32a

<400> 14
gtgatatctg atctgtctgg tggtggt 27

<210> 15
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pT7-7

<400> 15
cgcataatgga cccgatcgct ggtgct 26

<210> 16
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (-) of insertion into pT7-7

<400> 16
gaatttcctaa gcgtcaaacac cagc 24

<210> 17
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pT7-7

<400> 17
catatggaaat acgttggttc 19

<210> 18
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (-) of insertion into pT7-7

<400> 18
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<210> 19
<211> 103
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: sens DNA
coding TME2 + 5' Nde I site and 3' Hind III site

<400> 19
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ctgtggatga tgctgctgat ctctcaggct gaagcttaag ctt 103

<210> 20
<211> 103
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: sens DNA
anticoding TME2 + 3' Nde I site and 5' Hind III site

<400> 20
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cgtcagccag cagcaggaac agcagaacaa cgtattccat atg 103

<210> 21
<211> 68
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
sens oligonucleotide (+) coding for the synthesis
of TME2

<400> 21
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ctgtggat 68

<210> 22
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
sens oligonucleotide (-) coding for the synthesis
of TME2

<400> 22
aagcttaagc ttcagcctga gagatcagca gcatcatcca caggcaagac gaaacac 57

<210> 23
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pGEXKT without
the dp site

<400> 23
ggatccaaat acgttgttc 19

<210> 24
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide (+) of insertion into pGEXKT with
the dp site

<400> 24	
ggatccgacc cggaatacgt tggtc	25
<210> 25	
<211> 30	
<212> DNA	
<213> Artificial sequence	
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<223> Description of the artificial sequence: oligonucleotide (-) of insertion into pGEXKT with the dp site	
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<210> 26	
<211> 27	
<212> DNA	
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<223> Description of the artificial sequence: oligonucleotide (+) of insertion into pT7-7	
<400> 26	
cgcataatgga cccggaatac gttgttc	27
<210> 27	
<211> 27	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Description of the artificial sequence: oligonucleotide (-) of insertion into pT7-7	
<400> 27	
cagaattcct aagcttcagc ctgagag	27
<210> 28	
<211> 15	
<212> PRT	
<213> Artificial sequence	
<220>	
<223> Description of the artificial sequence: end of the GST followed by the thrombine site	
<400> 28	
Ser Asp Leu Ser Gly Gly Gly Gly Gly Leu Val Pro Arg Gly Ser	
1 5 10 15	15
<210> 29	
<211> 717	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Description of the artificial sequence: DNA coding for GST protein in the pGEXKT vector	

<400> 29

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ttgaaatatac	ttgaagaaaa	atatacgag	catttgatg	agcgcgtatg	aggtgataaa	120
tggcgaaaca	aaaagtttga	attgggtttg	gagtttccca	atcttcctta	ttatattgtat	180
ggtgatgtta	aattaacaca	gtctatggcc	atcatacggt	atatacgatg	caagcacaac	240
atgttgggtg	gttgcacaaa	agagcgtgca	gagattcaa	tgcttgaagg	agcggttttg	300
gatattagat	acgggtttc	gagaattgca	tatagtaaag	actttgaaac	tctcaaagtt	360
gatttctta	gcaagctacc	tgaaatgtcg	aaaatgttcg	aaagatcgtt	atgtataaa	420
acatatttaa	atggtgatca	tgtacccat	cctgacttca	tggtgtatga	cgctcttgat	480
gttggggat	acatggaccc	aatgtgcctg	gatgcgttcc	caaaaattgt	ttgtttaaa	540
aaacgtattg	aagctatccc	acaaattgtat	aagtacttga	aatccagcaa	gtatatacg	600
tggccttgc	agggctggca	agccacgtt	ggtgggtggcg	accatccctcc	aaaatcgat	660
ctgtctggtg	gtgggtggtg	tctggatccc	cgtggatccc	cgggaattca	tcgtgac	717

<210> 30

<211> 327

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: DNA
coding for the thioredoxine in the pET32a+ vector

<400> 30

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ccgattctgg	atgaaatcgc	tgacgaatat	cagggcaaac	tgaccgttgc	aaaactgaac	180
atcgatcaaa	accctggcac	tgcgcccggaa	tatggcatcc	gtggtatccc	gactctgctg	240
ctgttcaaaa	acggtgaagt	ggcggcaacc	aaagtgggtg	cactgtctaa	aggtcagttg	300
aaagagttcc	tcgacgctaa	cctggcc				327

<210> 31

<211> 4969

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmide
expressing pGEXKT

<400> 31

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<210> 32
 <211> 11800
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: plasmide
 expressing PET32a+

<400> 32

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actatggatg	aacgaaatag	acagatcg	gagatagg	cctca	taagcattt	2460
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<210> 34

<211> 813

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system
coding for fusion protein GST-DP-TME1

<400> 34

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ttggaaat	ttgaagaaaa	atatgaagag	catttgc	agcgcgtat	aggtgataaa	120
tggc	aaaagtttga	atgggttt	gagtttcc	atttccctt	ttatattgt	180
ggtgtatgtt	aattaacaca	gtctatggcc	atcatacg	atatagctg	caagcacaac	240
atgttgggt	gttgtccaaa	agagcgtg	gagatttca	tgc	ttgtgttgc	300
gatatttagat	acggtgtt	gagaattg	caat	tttgaaac	tctcaagtt	360
gat	tttctt	gcaagctt	aaaatgtcg	aaatcg	tatgtcataaa	420

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acatatttaa	atgggtatca	tgttaaccat	cctgacttca	tgttgttatga	cgctcttgat	480
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aaacgtattg	aagctatccc	acaaaattgat	aagtacttga	aatccagcaa	gtatatagca	600
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ctgtctggtg	gtgggtgtgg	tctggttccg	cgtggatccg	acccgatcgc	tggtgctcac	720
tggggtgttc	tggctggtat	cgcttacttc	tctatggttg	gtaactgggc	taaagttctg	780
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<210> 35
<211> 513
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression system
coding for fusion protein TrX-DP-TME1

<400> 35
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gacggggcga tcctcgtcga tttctggca gagtggtgcg gtccgtgcaa aatgatcgcc 120
ccgattctgg atgaaatcgc tgacgaatat cagggcaaac tgaccgttgc aaaactgaac 180
atcgatcaaa accctggcac tgcgccgaaa tatggcatcc gtggtatccc gactctgctg 240
ctgttcaaaa acggtgaagt ggcggcaacc aaagtgggtg cactgtctaa aggtcagttg 300
aaagagttcc tcgacgctaa cctggccggt tctggttctg gatctccaaa atcggatctg 360
tctggtgtg gtgggtgtct gggtccgcgt ggatccgacc cgatcgctgg tgctcactgg 420
ggtgttctgg ctggtatcgc ttacttctct atggttggta actgggctaa agttctgggt 480
gttctgctgc tgttcgcgtgg tggtgacgct tag 513

<210> 36
<211> 117
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression system
coding for fusion protein M-DP-TME1

<400> 36
atggacccga tcgctggtgc tcactgggt gttctggctg gtatcgctta cttctctatg 60
gttggtaact gggctaaagt tctggttgtt ctgctgctgt tcgctgggtg tgacgct 117

<210> 37
<211> 795
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression system
coding for fusion protein
GST-DP-TME2

<400> 37
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tggcgaaaca aaaagttga attgggtttg gagtttccca atcttcctta ttatattgat 180
ggtgatgtta aattaacaca gtctatggcc atcatacggtt atatagctga caagcacaaac 240
atgttgggtg gttgtccaaa agagcgtgca gagatttcaa tgcttgaagg agcgggtttg 300
gatatttagat acgggtttc gagaattgca tatagtaaag actttggaaac tctcaaagt 360
gattttctta gcaagctacc tgaatgctg aaaatgttcg aagatcggtt atgtcataaa 420
acatatttaa atgggtatca tgtaaccat cctgacttca tgggttatga cgctcttgat 480
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ctgtctggtg gtgggtgtgg tctggttccg cgtggatccg acccggaaata cggttctgt 720
ctgttcctgc tgctggctga cgctcgtgtt tgctctgccc tggtggatgat gctgctgatc 780

<210> 38
 <211> 486
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: expression system
 coding for fusion protein
 TrX-DP-TME2

<400> 38
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 ccgattctgg atgaaatcgc tgacgaatat cagggcaaac tgaccgttgc aaaactgaac 180
 atcgatcaaa accctggcac tgcgcccggaa tatggcatcc gtggtatccc gactctgctg 240
 ctgttcaaaa acggtgaagt ggcggcaacc aaagtgggtg cactgtctaa aggtcagttg 300
 aaagagttcc tcgacgctaa cctggccggg tctgggtctg gatctgatct gtctgggtg 360
 ggtgggtgtc tggatcccgac ccggaaatacg ttgttctgct gttcctgctg 420
 ctggctgacg ctcgtgtttg ctcttcgtc tggatgatgc tgctgatctc tcaggctgaa 480
 gcttag 486

<210> 39
 <211> 99
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: expression system
 coding for fusion protein M-DP-TME2

<400> 39
 atggaccggg aatacgttgt tctgctgttc ctgctgctgg ctgacgctcg tgtttgcct 60
 tgccctgtgaa tgatgctgct gatctctcag gctgaagct 99

<210> 40
 <211> 5082
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: expression vector
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<400> 40
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 tctggataat gttttttcgccgacatcat aacgggtctg gcaaatattc tgaaatgagc 180
 tggatcaat taatcatcggt ctcgtataat gtgtggatt gtgagcggat aacaatttca 240
 cacaggaaac agtatttcgt tcccctatac taggttattt gaaaattaaag ggccttgc 300
 aaccactcg acttcttttggaaatcttgcg aagaaaaata tgaagagcat ttgtatgagc 360
 gcgatgaagg tgataaaatgg cgaaacaaaa agtttgaatt gggtttggag tttcccaatc 420
 ttccttatta tattgtatggt gatgtttaat taacacatgc tatggccatc atacgttata 480
 tagctgacaa gcacaacatg ttgggtgggt gtccaaaaga gctgtcagag atttcaatgc 540
 ttgaaggagc gttttggat attagatacg gtgtttcgag aattgcataat agtaaagact 600
 ttgaaactct caaagttgtat tttcttagca agctacatgc aatgctgaaa atgttgcag 660
 atcgtttatg tcataaaaaca tattttaaatg gtgatcatgt aacccatcct gacttcatgt 720
 tgtatgacgc tcttgcgtt gttttataca tggacccat gtgcctggat gcgttccaa 780
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tagcgat	ggagtgtat	attcttga	acgaaagg	ctcgat	gcctatttt	1320
ataggtaat	gtcatgata	taatggtt	ttagacgt	ggtggcact	ttcgggaaa	1380
tgtgcgcg	accctattt	gtttat	ctaaatacat	tcaaataatgt	atccgctcat	1440
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tacgatgc	ccatct	caacgt	tttttgc	tttttgc	gcccgttgc	4980
cccacgaga	atccgac	ttgtt	tttttgc	tttttgc	aagctggct	5040
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<210> 41
 <211> 5064
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: expression vector
 pGEXKT-dp-Pt(TME2)

<400> 41

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<210> 42

<211> 5918

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector
pET32a-dp-Pt(TME1)

<400> 42

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<210> 43
<211> 5891
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression vector
pET32a-dp-Pt(TME2)

<400> 43

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gaaaacgttc	ttcggggcga	aaactctcaa	ggatcttacc	gtgttgaga	tccagttcga	5160
tgttaaccac	tctgcaccc	aactgtatctt	cagcatcttt	tactttcacc	agcgtttctg	5220
ggtgagcaaa	aacaggaaag	caaaatgccg	caaaaagggg	aataaggcgc	acacggaaat	5280
gttgaatact	catactcttc	cttttcaat	attattgaag	catttatcag	gttattgtc	5340
tcatgagcgg	atacatattt	gaatgtatctt	agaaaaataaa	acaatagggg	gttccgcgc	5400
catttccccg	aaaagtgc	cctgaaattt	taaacgttta	tattttgtta	aaattcgcgt	5460
taaatttttg	ttaaatcagc	tcattttta	accaataggg	cggaaatcggc	aaaatccctt	5520
ataaaatcaaa	agaatagacc	gagatagggt	tgagtgttgt	tccagtttgg	aacaagagtc	5580
cactattaaa	gaacgtggac	tccaaacgtca	aagggcggaa	aaccgtctat	cagggcgtat	5640
gcccactacg	tgaaccatca	ccctaataca	gttttttgg	gtcgagggtc	cgtaaagcac	5700
taaattcgaa	ccctaaagggg	agccccgtat	ttagagctt	acggggaaag	ccggcgaacg	5760
tggcgagaaa	ggaagggaaag	aaagcgaaag	gagcgggcgc	tagggcgtg	gcaagtgtag	5820
cggtcacgtc	gcgcgttaacc	accacacccg	ccgcgtttaa	tgcggcgct	caggcgcgt	5880
cccatttcggcc	a					5891

<210> 44
<211> 2617
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: expression vector
pT7-7-dp-Pt(TME1)

<400> 44	aattctcatg	tttgacagct	tatcatcgat	gataagcttg	ggctgcaggt	cgactctaga	60
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acttttagccc	agtattaccaac	catagagaag	taagcgatac	cagccagaac	accccgagtga	180	
gcaccagcga	tcgggtccat	atgtatatact	ccttcttaaa	gttaaacaaa	attatttcta	240	
gagggaaacc	gttgggtgtct	ccctatagtg	agtcgttatta	atttcgaagt	ctatcagaag	300	
ttcgaatcgc	tgggcctcgc	gcgtttcggt	gatgacggtg	aaaacctctg	acacatgcag	360	
ctcccggaga	cggtcacagc	ttgtctgtaa	gcggatgccc	ggagcagaca	agcccgtag	420	
ggcgcgtcag	cgggtgttgg	cgggtgtcgg	ggcgcagcca	tgaccgcgtc	acgttagcgat	480	
agcggagtgt	atatactggc	ttaactatgc	ggcatcagag	cagattgtac	tgagagtgca	540	
ccataggaag	atttcccgga	agatcttcct	atgcggtgtg	aaataccgca	cagatgcgta	600	
aggagaaaaat	accgcatcag	gcgcttcc	gcttcctcgc	tcactqactc	gctgcgctcg	660	

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gtcgttcggc	tgcggcgagc	ggtatcagct	cactcaaagg	cggtaaatacg	gttatccaca	720
gaatcagggg	ataacgcagg	aaagaacatg	tgagcaaaag	gccagaaaa	ggccaggaac	780
cgtaaaaaagg	ccgcgttgct	ggcgttttc	cataggctcc	ccccccctga	cgagcatcac	840
aaaaatcgac	gctcaagtca	gaggtggcga	aacccgacag	gactataaaag	ataccaggcg	900
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ctgtccgcct	ttctcccttc	gggaagcgtg	gchgcttctc	aatgctcagc	ctgttaggtat	1020
ctcagttcgg	tgttaggtcgt	tcgctccaag	ctgggtctgt	tgcacgaacc	ccccgttcag	1080
cccgaccgct	gccccttatac	cgttaactat	cgtcttgagt	ccaaccgggt	aagacacgac	1140
ttatcgccac	tggcagcagc	cactggtaac	aggattagca	gagcgaggt	tgtaggcggt	1200
gctacagagt	tcttgaagtg	gtggcctaac	tacggctaca	ctagaaggac	agtatttggt	1260
atctgcgctc	tgctgaagcc	agttaaccttc	ggaaaaaagag	ttggtagctc	ttgatccggc	1320
aaacaaacca	ccgctggtag	cggtggtttt	tttgtttgca	agcagcagat	tacgcgcaga	1380
aaaaaaggat	ctcaagaaga	tcccttgcata	ttttctacgg	ggctctgacgc	tcagtgaaac	1440
gaaaactcac	gttaagggtat	tttggtcatg	agattatcaa	aaaggatctt	cacctagatc	1500
cttttaattc	ttgaagacga	aaggggctcg	tgataccgc	atttttatag	gttaatgtca	1560
tgataataatc	gttttcttag	acgtcagggt	gcacttttcg	ggggaaatgtg	cgcggaaaccc	1620
ctatttgttt	atttttctaa	atacattcaa	atatgtatcc	gctcatgaga	caataaccct	1680
gataaaatgct	tcaataaatat	tgaaaaaagga	agagtatgag	tattcaacat	ttccgtgtcg	1740
cccttattcc	cttttttgcg	gcattttgccc	ttcctgtttt	tgctcacccca	gaaacgctgg	1800
tgaaagtaaa	agatgcgtaa	gatcagttgg	gtgcacgagt	gggttacatc	gaactggatc	1860
tcaacagcgg	taagatccctt	gagagtttc	gccccgaaga	acgtttcca	atgatgagca	1920
cttttaaagt	tctgctatgt	ggcgcggat	tatcccgtgt	tgacgcccggg	caagagcaac	1980
tcggtcgccc	catacactat	tctcagaatg	acttggttga	gtactcacc	gtcacagaaa	2040
agcatcttac	ggatggcatg	acagtaagag	aattatgcag	tgctgccata	accatgagtg	2100
ataacactgc	ggccaactta	cttctgacaa	cgatcgagg	accgaaggag	ctaaccgcctt	2160
ttttgcacaa	catggggat	catgtactc	gccttgatcg	ttggaaaccg	gagctgaatg	2220
aagccatacc	aaacgacgag	cgtgacacca	cgatgcctgt	agcaatggca	acaacgttgc	2280
gcaaactatt	aactggcgaa	ctacttactc	tagctcccg	gcaacaatta	atagactgga	2340
tggaggcgg	taaagtgtca	ggaccacttc	tgcgctcgcc	ccttccggct	ggctgggtta	2400
ttgctgataa	atctggagcc	ggtgagcgtg	ggtctcgccg	tatcattgtca	gcactggggc	2460
cagatggtaa	gccctcccg	atcgtagtt	tctacacgac	ggggagtcag	gcaactatgg	2520
atgaacgaaa	tagacagatc	gctgagatag	gtgcctcact	gattaagcat	tggtaactgt	2580
cagaccaagt	ttactcataat	atactttaga	ttgattt			2617

<210> 45

<211> 2599

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector
pT7-7-dp-Pt(TME2)

<400> 45

aattctcatg	tttgacagct	tatcatcgat	gataagctt	ggctgcaggt	cgactctaga	60
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caagagcaaa	cacgagcgtc	agccagcagc	aggaacacga	gaacaacgt	ttccgggtcc	180
atatgtatat	ctccttctta	aagttaaaca	aaattatttc	tagagggaaa	ccgttgggtgt	240
ctccctatag	tgagtcgtat	taatttcgaa	gtctatcaga	agttcgaatc	gctgggcctc	300
gcgcgtttcg	gtgatgcacgg	tggaaaaccc	tgacacatgc	agctcccgg	gacgggtcaca	360
gcttgtctgt	aaggcgatgc	cgggagcaga	caagccgtc	agggcgcgtc	agcgggtgtt	420
ggcgggtgtc	ggggcgcacg	catgaccgg	tcacgtagcg	atagcggat	gtatatactg	480
gcttaactat	gcggcatcag	agcaggatgt	actgagatgt	cacccatagga	agatttccg	540
gaagatcttc	ctatgcgttg	tggaaaatacc	cacagatgc	taaggagaaa	ataccgcac	600
aggcgctctt	ccgcttcc	gctcaactgac	tcgctcgct	cggtcggtt	gctgcggcga	660
gcggtatcat	ctcactaaa	ggcgtaata	cggttatcca	cagaatcagg	ggataacgca	720
ggaagaagaaca	tgtgagaaa	aggccagca	aaggccagga	accgtaaaaaa	ggccgcgtt	780
ctggcgtttt	tccataggct	ccgcccccc	gacgagcatc	acaaaaatcg	acgctcaagt	840
cagaggtggc	gaaaccggac	aggactataa	agataaccagg	cgtttcccc	tggaaactcc	900
ctcggtcgct	ctccgttcc	gaccctggc	cttaccggat	acctgtccgc	ctttccct	960
tcgggaagcg	tggcgctt	tcaatgtca	cgctgttagt	atctcagtt	ggtgttaggt	1020
gttcgctcca	agctggctg	tgtgcacgaa	ccccccgttc	agcccggacc	ctgcgcctta	1080
tccggtaact	atcgcttga	gtccaaaccc	gtaagacacg	acttatacgcc	actggcagca	1140
gccactggta	acaggattag	cagagcgg	tatgttaggc	gtgctacaga	gttcttgaag	1200
tggtggcccta	actacggcta	cactagaagg	acagtatttg	gtatctgcgc	tctgctgaag	1260
ccagttacact	tcggaaaaaa	agtggtagc	tcttgcattcg	gcaaaacaaac	caccgcgtgt	1320
agcggtgggt	tttttggttt	caagcagcag	attacgcgc	gaaaaaaaagg	atctcaagaa	1380

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gatccttga tctttctac ggggtctgac gctcagtgaa acgaaaactc acgttaaggg 1440
attttggtca tgagattatc aaaaaggatc ttcacctaga tccttttaat tcttgaagac 1500
gaaagggcct cgtgatacgc ctattttat aggttaatgt catgataata atggttctt 1560
agacgtcagg tggcacttt cggggaaatg tgccggaac ccctattgt ttattttct 1620
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attaaaaaag gaagagatgt agtattcaac atttccgtgt cgcccttatt ccctttttg 1740
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aagatcagg ggggtgcacga gtgggttaca tcgaactgga tctcaacagc ggtaagatcc 1860
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attctcagaa tgacttgggtt gagtaactcac cagtcacaga aaagcatctt acggatggca 2040
tgacagtaag agaattatgc agtgctgcca taaccatgag tgataaacact gcccact 2100
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aactacttac tctagcttcc cgccaaat taatagactg gatggaggcg gataaagttg 2340
caggaccact tctgcgtcg gcccttccgg ctggctgggtt tattgctgat aaatctggag 2400
ccggtgagcg tgggtctcgc ggtatcattt cagcactggg gccagatggt aagccctccc 2460
gtatcgtagt tatctacacg acggggagtc aggcaactat ggatgaacga aatagacaga 2520
tcgctgagat aggtgcctca ctgattaagc attggtaact gtcagaccaa gtttactcat 2580
atatacttta gattgattt 2599

<210> 46

<211> 271

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: fusion protein
GST-DP-TME1

<400> 46

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190

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Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly
210 215 220

Gly Gly Gly Leu Val Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His
225 230 235 240

Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp
245 250 255

Ala Lys Val Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
260 265 270

<210> 47

<211> 265

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: fusion protein
GST-DP-TME2

<400> 47

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly
210 215 220

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Gly Gly Gly Leu Val Pro Arg Gly Ser Asp Pro Glu Tyr Val Val Leu
225 230 235 240
Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys Ser Cys Leu Trp Met
245 250 255
Met Leu Leu Ile Ser Gln Ala Glu Ala
260 265

<210> 48
<211> 170
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
TrX-DP-TME1

<400> 48
Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
1 5 10 15
Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
20 25 30
Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
35 40 45
Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
50 55 60
Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
65 70 75 80
Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
85 90 95
Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
100 105 110
Ser Gly Ser Pro Lys Ser Asp Leu Ser Gly Gly Gly Gly Leu Val
115 120 125
Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala
130 135 140
Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val
145 150 155 160
Val Leu Leu Leu Phe Ala Gly Val Asp Ala
165 170

<210> 49
<211> 161
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: fusion protein
TrX-DP-TME2

<400> 49
Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
1 5 10 15

Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
 20 25 30
 Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
 35 40 45
 Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
 50 55 60
 Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
 65 70 75 80
 Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
 85 90 95
 Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
 100 105 110
 Ser Gly Ser Asp Leu Ser Gly Gly Gly Gly Leu Val Pro Arg Gly
 115 120 125
 Ser Asp Pro Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala
 130 135 140
 Arg Val Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu
 145 150 155 160
 Ala

<210> 50
 <211> 39
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: fusion protein
 M-DP-TME1

<400> 50
 Met Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala
 1 5 10 15
 Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu
 20 25 30
 Leu Phe Ala Gly Val Asp Ala
 35

<210> 51
 <211> 33
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: fusion protein
 M-DP-TME2

<400> 51
 Met Asp Pro Glu Tyr Val Val Leu Leu Phe Leu Leu Ala Asp Ala
 1 5 10 15
 Arg Val Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu
 20 25 30

Ala

<210> 52
 <211> 239
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 glutathione transferase (GST)

<400> 52
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly
 210 215 220
 Gly Gly Gly Leu Val Pro Arg Gly Ser Pro Gly Ile His Arg Asp
 225 230 235

<210> 53
 <211> 170
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 thioredoxin (Trx)

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<400> 53
Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
1 5 10 15
Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
20 25 30
Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
35 40 45
Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
50 55 60
Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
65 70 75 80
Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
85 90 95
Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
100 105 110
Ser Gly Ser Pro Lys Ser Asp Leu Ser Gly Gly Gly Gly Leu Val
115 120 125
Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala
130 135 140
Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val
145 150 155 160
Val Leu Leu Leu Phe Ala Gly Val Asp Ala
165 170